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Result No.	Score	Query Match	Length	DB	ID	Description
1	56.5	29.4	111	5	O96868	O96868 heliocidari
2	56.5	29.4	111	5	O96869	O96869 heliocidari
3	56.5	29.4	126	16	Q8VJ53	Q8VJ53 mycobacteri
4	56.5	29.4	223	16	Q10843	Q10843 mycobacteri
5	56.5	29.4	328	6	O95MP1	O95mp1 bos taurus
6	56.5	29.4	565	2	Q9ZNN9	Q9znn9 comamonas t
7	56.5	29.4	584	2	Q9S150	Q9s150 comamonas t
8	56.5	29.4	680	5	Q8WSN8	Q8wsn8 caenorhabdi
9	55	28.6	515	8	Q8SME7	Q8sme7 globba plat
10	55	28.6	694	10	Q9XF52	Q9xf52 arabidopsiis
11	54.5	28.4	191	6	Q9N2C2	Q9n2c2 oryctolagus
12	54	28.1	287	3	Q9UT16	Q9ut16 schizosacch
13	54	28.1	316	11	Q9AAP0	Q9aap0 caulobacteri
14	53.5	27.9	179	11	Q8R057	Q8r057 mus musculus
15	53.5	27.9	328	11	Q924K1	Q924k1 mus musculu
16	53.5	27.9	372	6	Q95MN8	Q95mn8 papio cynoc

OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas
OX NCBI_TaxID=285;

DR PRINTS; PR00179; LIPOCALIN.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 191 AA; 21444 MW; 1424BD9878512F61 CRC64;

Query Match 28.4%; Score 54.5; DB 6; Length 191;
Best Local Similarity 33.3%; Pred. No. 4.6;
Matches 10; Conservative 6; Mismatches 13; Indels

QY 5 WGD^TLNCWMLSA-FSRYARCLAE^{GHDGPTQ} 33
||| : | : : || | - | - |
Db 112 WG^{SYSV}VVVVD^{TDYKEFALL}YSEGAKGPQ 141

RESULT 12

Q9UT16	PRELIMINARY;	PRT;	287 AA.
ID	Q9UT16		
OC	Q9UT16;		
OC	Q9UT16;		
DT	01-MAY-2000 (IREMBLrel. 13, Created)		
DT	01-MAY-2000 (IREMBLrel. 13, Last sequence update)		
DT	01-MAY-2000 (IREMBLrel. 13, Last annotation update)		
DE	01-MAY-2000 (IREMBLrel. 13, Last annotation update)		
DE	Yeast ap12 protein precursor homolog.		
GN	SPAC9.12C.		
OS	Schizosaccharomyces pombe (Fission yeast).		
OS	Schizosaccharomycetes		
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;		
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;		
OC	Schizosaccharomycetes.		
OX	NCBI_TaxID:4896;		
OX	NCBI_TaxID:4896;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
NC	STRAIN=972H;		
NC	STRAIN=972H;		
RL	Wedler H., Duesterhoeft A., Lyne M.H., Rajandream M.		
RL	Submitted (Oct-1999) to the EMBL/GenBank/DBJ database		
RL	EMBL; AL112164; CAB57430.1;		
DR	SEQUENCE 287 AA; 33149 MW; 21F78CCD7B2FFD97 CRC64		
DR	SEQUENCE 287 AA; 33149 MW; 21F78CCD7B2FFD97 CRC64		

Query Match 28.1%; Score 54; DB 3; Length 287;
Best Local Similarity 47.4%; Pred. No. 8.3;
Matches 9; Conservative 2; Mismatches 8; Indels

```

QY      5 WGDTLNCWMLSAFSRYARC 23
      | :| | | | :| | | | .|
Db     198 WLSSLNSWQLAAFERSVSC 216

```

RESULT 13

Q9AAP0	PRELIMINARY;	PRT;	316 AA.
Q9AAP0;			
01-JUN-2001	(TREMBLrel. 17, Created)		
01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	Hypothetical protein CC0557.		
CC0557.			
OS	Caulobacter crescentus.		
OC	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;		
OC	Caulobacter.		
OX	NCBI_TaxID=155892;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 19089 / CB15;		
RX	MEDLINE=21173698; PubMed=11259647;		
RA	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,		
RA	Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,		
RA	Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,		
RA	DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,		
RA	Kolony J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,		
RA	Utterback T., Tran K., Wolf A., Vamaichevan J., Ermolaeva M., White O.,		
RA	Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;		
RT	"Complete genome sequence of <i>Caulobacter crescentus</i> ."		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).		
DR	EMBL: AE005729; AAK22543.1; --		
DR	TIGR: CC0557; --		
KW	Hypothetical protein; Complete proteome.		

SQ	SEQUENCE	316 AA;	35026 MW;	41C4289216FED963	CRC64;
	Query Match		28.13;	Score 54;	DB 16;
	Best Local Similarity		56.28;	Pred. No. 9.2;	Length 316;
	Matches	9;	Conservative	2;	Mismatches 5; Indels

QY	6	GDTLNCWMLSAFSRYA	21
Db	301	GDILSCWKLGAVPRYS	316

RESULT 14

Q8R057	PRELIMINARY;	PRT;	179 AA.
ID	Q8R057		
AC	Q8R057;		
DT	01-JUN-2002 (TReMBUrel. 21, Created)		
DT	01-JUN-2002 (TReMBUrel. 21, Last sequence update)		
DT	01-JUN-2002 (TReMBUrel. 21, Last annotation update)		
DE	Similar to aryl-Hydrocarbon interacting protein-like 1.		
DE	Mus musculus (Mouse).		
OS	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
QC	NCBI_TaxID:10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=EYE.		
RA	Strausberg R.;		
RL	Submitted (APR-2002) to the EMBL/GenBank/DDJB databases.		
DR	EMBL; BC028285; AAH28285.1; -		
SQ	SEQUENCE 179 AA; 20424 MW; 32ED79C343761A10 CRC64;		

Query Match	27.9%	Score 53.5;	DB 11;	Length 179;
Best Local Similarity	44.8%	Pred. No. 6.1;		
Matches 13; Conservative	4;	Mismatches	11;	Indels 1;
				Gaps 1;

QY 4 FWGDTLNCWMLSAFSRYARCLAEHGDGPT 32
|||::: |||: |||: |||: |||

Db 87 FWCDTIHNGVYPMLSRSLRQVAEGKD-PT 114

RESULT 15

Q924K1	PRELIMINARY;	PRT;	328 AA.
ID	Q924K1		
AC	Q924K1;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Aryl-hydrocarbon interacting protein-like 1.		
GN	AIPL1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21313649; PubMed=11420621;		
RA	Sohocki M.M., Sullivan L.S., Tirpak D.L., Daiger S.P.;		
RT	"Comparative analysis of aryl-hydrocarbon receptor interacting		
RT	protein-like 1 (Aipl1), a gene associated with inherited retinal		
RT	disease in humans.;"		
RL	Mamm. Genome 12:566-568(2001).		
RL	EMBL; AF296412; AAK7956.1; "		
DR	MGD; MGI:2148800; Aipl1		
DR	InterPro; IPR001440; TPR.		
DR	Prfam; PF00515; TPR; 2.		
SQ	SEQUENCE 328 AA; 38303 MW; 5D34AAE530A325A7 CRC64;		

Query Match	27.9%	Score 53.5;	DB 11;	Length 328;
Best Local Similarity	44.8%;	Pred. No. 11;		
Matches 13;	Conservative	4;	Mismatches 11;	Indels 1;
				Gaps 1;

Qy 4 FWGDTLNCWMLSAFSRYARCLAEAGHDGPT 32

Thu May 29 16:01:03 2003

us-09-989-481-4.rspt

Page 6

Db 87 FWCDTHTGVPMLSRSLRQVAREKD-PT 114

Search completed: May 29, 2003, 15:45:02
Job time : 82 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:34:05 ; Search time 22 seconds
(without alignments)
62.214 Million cell updates/sec

Title: US-09-989-481-4

Perfect score: 192

Sequence: 1 LGTFWGDTLNCWMLSAFSRYARCLAEHGDPTQ 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	59	30.7	910	1	IMB2_SCHPO
2	53.5	27.9	328	1	AIPL_RAT
3	53.5	27.9	384	1	AIPL_HUMAN
4	52	27.1	563	1	LIP1_GEOCN
5	51	26.6	418	1	CGAL_XENLA
6	51	26.6	474	1	ASCB_ECOLI
7	51	26.6	1207	1	EGF_HUMAN
8	49.5	25.8	355	1	GBA2_NEUCR
9	49.5	25.8	847	1	ENV_HV1S1
10	49	25.5	282	1	APAH_BURMA
11	49	25.5	282	1	APAH_BURPS
12	48	25.0	229	1	PEPE_ECOLI
13	48	25.0	472	1	HEAD_BPGAL
14	48	25.0	1959	1	AGRI_RAT
15	47	24.5	690	1	PPK_PSEAE
16	47	24.5	3433	1	POLG_KUNJM
17	46.5	24.2	729	1	NARB_SYNP7
18	46.5	24.2	895	1	ODP1_ALCEU
19	46	24.0	182	1	C560_CAEEL
20	46	24.0	184	1	C560_CAEER
21	46	24.0	361	1	COOH_RHORU
22	46	24.0	449	1	HEAD_BPG03
23	46	24.0	1550	1	GLTB_SYNY3
24	46	24.0	1822	1	ITB4_HUMAN
25	45.5	23.7	126	1	FY81_XYLFA
26	45.5	23.7	614	1	VAAL_DROME
27	45	23.4	114	1	RSN_MOUSE
28	45	23.4	158	1	NEU4_ONCKE
29	45	23.4	334	1	GBLP_ORYSA
30	45	23.4	404	1	VE2_HPV60
31	45	23.4	698	1	PPK_XYLFA
32	45	23.4	1597	1	SOL_DROME
33	45	23.4	3038	1	TRIO_HUMAN

RESULT 1

ID	IMB2_SCHPO	STANDARD	PRT	910 AA
AC	014089			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Putative importin beta-2 subunit (Karyopherin beta-2 subunit)			
DE	(Importin 104) (Transportin) (TRN).			
GN	SPAC2F3.06C.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetes.			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=21848401; PubMed=11859360;			
RA	WOOD V., William R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	SGouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson A.,			
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,			
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
RA	Skilton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,			
RA	Weltjens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,			
RA	Borzum K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,			
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,			
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,			
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
RA	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,			
RA	Daga R.R., Cruzado J., Jimenez J., Sanchez M., del Rey F., Benito J.,			
RA	Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,			
RA	Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,			
RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;			
RL	"The genome sequence of Schizosaccharomyces pombe.";			
RL	Nature 415:871-880(2002).			
CC	-1- FUNCTION: REQUIRED FOR IMPORT OF MRNA BINDING PROTEINS. BINDS TO			
CC	NUCLEOPORINS (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE IMPORTIN BETA FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 IMPORTIN N-TERMINAL DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 9 HEAT REPEATS.			
CC	-----			
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CC	use by non-profit institutions as long as its content is in no way			

P06935 w genome po
Q29487 felis silve
Q08869 pasteurella
P80147 sus scrofa
P50534 rattus norv
P31404 bos taurus
P38606 homo sapien
P50516 mus musculu
Q29048 sus scrofa
P15145 sus scrofa
P51527 meleagris g
P00746 homo sapien

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DR EMBL: Z99165; CAB16272.1; -
DR HSSP: Q29273; LOBK.
DR PROSITE; PS0077; HEAT_REPEAT; FALSE_NEG.
DR PROSITE; PS0166; IMPORTIN_B_NT; FALSE_NEG.
KW Hypothetical protein; Transport; Protein transport; Repeat.
FT DOMAIN 34 122 IMPORTIN N-TERMINAL.
FT REPEAT 127 164 HEAT 1.
FT REPEAT 174 211 HEAT 2.
FT REPEAT 299 336 HEAT 3.
FT REPEAT 410 447 HEAT 4.
FT REPEAT 451 488 HEAT 5.
FT REPEAT 497 534 HEAT 6.
FT REPEAT 538 575 HEAT 7.
FT REPEAT 579 608 HEAT 8.
FT REPEAT 609 640 HEAT 9.
FT REPEAT 641 672 HEAT 10.
FT DOMAIN 366 385 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 910 AA; 101718 MW; 4939CD9B09877208 CRC64;

Query Match 30.7%; Score 59; DB 1; Length 910;
Best Local Similarity 40.9%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 8 TLNCWMLSAFSAFYARCLAEHGD 29
Db 473 TITCWTGLGRYSKWASCLESEED 494

RESULT 2
AIPL_RAT
ID AIPL_RAT STANDARD; PRT; 328 AA.
AC Q9JL69;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aryl-hydrocarbon interacting protein-like 1.
GN AIPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082814; PubMed=10615133;
RA Schocki M.M., Bowne S.J., Sullivan L.S., Blackshaw S., Cepko C.L.,
RA Payne A.M., Bhattacharya S.S., Khalil Q., Mehdi Q., Birch D.G.,
RA Harrison W.R., Elder F.F.B., Heckenlively J.R., Daiger S.P.;
RA "Mutations in a novel photoreceptor-pineal gene on 17p cause Leber
congenital amaurosis";
RL Nat. Genet. 24:79-83(2000).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RETINA.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -!- DATABASE: NAME-Mutations of the AIPL gene.
CC NOTE-Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/aiplmut.htm".

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CC or send an email to license@isb-sib.ch).

DR EMBL: AF180340; AAF26707.1; -
DR InterPro: IPR001179; FKBP_PPIase.
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR; 2.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
DR PROSITE; PS00509; FKBP_PPIASE_3; FALSE_NEG.
KW Repeat; TPR repeat.
FT DOMAIN 53 145 PPIASE, FKBP-TYPE.
FT REPEAT 230 263 TPR 1.
FT REPEAT 264 297 TPR 2.
FT VARIANT 90 90 D -> H.
FT VARIANT 239 239 /FTIG=VAR_010140.
FT C -> R (IN LCA4).
FT /FTIG=VAR_010139.
SQ SEQUENCE 384 AA; 43596 MW; B116AA0724BAF9EA CRC64;

FT DOMAIN 53 145 PPIASE, FKBP-TYPE.
FT REPEAT 230 263 TPR 1.
FT REPEAT 264 297 TPR 2.
SQ SEQUENCE 328 AA; 38294 MW; E9BC3A4084F64A0E CRC64;

Query Match 27.9%; Score 53.5; DB 1; Length 328;
Best Local Similarity 44.8%; Pred. No. 4.1;
Matches 13; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 4 FWGDTLNCWMLSAFSAFYARCLAEHGDGPT 32
Db 87 FWCDTIHTGVYPMLSRSLRQVAEGKD-PT 114

RESULT 3
AIPL_HUMAN
ID AIPL_HUMAN STANDARD; PRT; 384 AA.
AC Q9NZN9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aryl-hydrocarbon interacting protein-like 1.
GN AIPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., VARIANT HIS-90, AND VARIANT LCA4 ARG-239.
RX MEDLINE=20082814; PubMed=10615133;
RA Schocki M.M., Bowne S.J., Sullivan L.S., Blackshaw S., Cepko C.L.,
RA Payne A.M., Bhattacharya S.S., Khalil Q., Mehdi Q., Birch D.G.,
RA Harrison W.R., Elder F.F.B., Heckenlively J.R., Daiger S.P.;
RA "Mutations in a novel photoreceptor-pineal gene on 17p cause Leber
congenital amaurosis";
RL Nat. Genet. 24:79-83(2000).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RETINA.
CC -!- DISEASE: DEFECTS IN AIPL ARE A CAUSE OF LEBER CONGENITAL
CC AMAUROSIS TYPE 4 (LCA4), A DISEASE CHARACTERIZED BY TOTAL
CC BLINDNESS OR GREATLY IMPAIRED VISION WITH LOSS OF CENTRAL VISION.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -!- DATABASE: NAME-Mutations of the AIPL gene.
CC NOTE-Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/aiplmut.htm".

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DR EMBL: AF180472; AAF26708.1; -
DR Genew; HGNC:359; AIPL1.
DR MIM; 604392; -
DR InterPro: IPR001179; FKBP_PPIase.
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR; 2.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
DR PROSITE; PS00509; FKBP_PPIASE_3; FALSE_NEG.
KW Repeat; TPR repeat; Disease mutation; Vision.
FT DOMAIN 53 145 PPIASE, FKBP-TYPE.
FT REPEAT 230 263 TPR 1.
FT REPEAT 264 297 TPR 2.
FT VARIANT 90 90 D -> H.
FT VARIANT 239 239 /FTIG=VAR_010140.
FT C -> R (IN LCA4).
FT /FTIG=VAR_010139.
SQ SEQUENCE 384 AA; 43596 MW; B116AA0724BAF9EA CRC64;

Query Match 27.9%; Score 53.5; DB 1; Length 384;
 Best Local Similarity 40.0%; Pred. No. 4.7;
 Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Oy 4 FWDGTLNCWMLSAFSAFYARCLAEHGDGPTQ 33
 |||::: : |||::: |||::: |||:::
 Db 87 FWCDDTHTGVYPIILSRSLQMAQCKD-PTE 115

RESULT 4

LIPI_GEOCN STANDARD; PRT; 563 AA.
 AC P17573;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Lipase 1 precursor (EC 3.1.1.3).
 OS Lip1.
 OS Geotrichum candidum (Oospora lactis).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Galactomyces.
 OX NCBI_Taxid-273117;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-ATCC 34614;
 RX MEDLINE-90110016; PubMed-2481674;
 RA Shimada Y., Sugihara A., Tomimaga Y., Iizumi T., Tsunasawa S.;
 RT "cDNA molecular cloning of Geotrichum candidum lipase.";
 RL J. Biochem. 106:383-388(1989).
 RN [2]
 RP SIMILARITY TO CARBOXYLESTERASES.
 RX MEDLINE-90328988; PubMed-2115773;
 RA Slabas A.R., Windust J., Sidebottom C.M.;
 RT "Does sequence similarity of human choline esterase, Torpedo
 acetylcholine esterase and Geotrichum candidum lipase reveal the
 active site serine residue?";
 RL Biochem. J. 269:279-280(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-91287805; PubMed-2062369;
 RA Schrag J.D., Li Y., Wu S., Cysler M.;
 RT "Ser-His-Glu triad forms the catalytic site of the lipase from
 Geotrichum candidum.";
 RL Nature 351:761-765(1991).
 CC -1- FUNCTION: THE EXTRACELLULAR LIPASE PRODUCED BY G. CANDIDUM
 HYDROLYZES ALL ESTER BONDS IN TRIGLYCERIDE AND DISPLAYS A HIGH
 AFFINITY FOR TRIOLEIN.
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 fatty acid anion.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR PIR: JQ0022; ACUGC.
 DR PDB: 1THG; 31-OCT-93.
 DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase; Lipid degradation; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 563
 FT MOD_RES 20 20
 FT ACT_SITE 236 236
 FT ACT_SITE 373 373
 FT ACT_SITE 482 482
 FT DISULFID 80 124
 FT DISULFID 295 307
 FT CARBOHYD 302 302
 FT CARBOHYD 383 383
 FT STRAND 23 26
 FT TURN 27 29
 FT STRAND 30 33
 FT STRAND 33 33
 FT STRAND 35 35
 FT TURN 37 37
 FT STRAND 38 38
 FT TURN 39 39
 FT STRAND 40 40
 FT HELIX 47 47
 FT STRAND 54 54
 FT TURN 56 56
 FT TURN 57 57
 FT TURN 69 69
 FT STRAND 71 72
 FT STRAND 74 74
 FT STRAND 77 77
 FT STRAND 79 79
 FT STRAND 85 85
 FT HELIX 96 96
 FT HELIX 98 98
 FT HELIX 101 101
 FT HELIX 104 104
 FT TURN 113 113
 FT TURN 114 114
 FT TURN 120 120
 FT STRAND 126 126
 FT STRAND 132 132
 FT TURN 133 133
 FT TURN 137 137
 FT STRAND 141 141
 FT TURN 147 147
 FT TURN 151 151
 FT TURN 152 152
 FT HELIX 156 156
 FT HELIX 163 163
 FT HELIX 171 171
 FT TURN 172 172
 FT STRAND 177 177
 FT TURN 181 181
 FT HELIX 186 186
 FT HELIX 194 194
 FT TURN 200 200
 FT TURN 202 202
 FT HELIX 204 204
 FT TURN 223 223
 FT TURN 224 224
 FT STRAND 225 225
 FT TURN 235 235
 FT TURN 236 236
 FT HELIX 237 237
 FT TURN 250 250
 FT TURN 251 251
 FT TURN 254 254
 FT TURN 256 256
 FT STRAND 259 259
 FT STRAND 263 263
 FT STRAND 267 267
 FT HELIX 285 285
 FT TURN 294 294
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 FT TURN 298 298
 FT TURN 301 301
 FT HELIX 310 310
 FT HELIX 313 313
 FT TURN 329 329
 FT TURN 331 331
 FT HELIX 334 334
 FT TURN 337 337
 FT TURN 351 351
 FT HELIX 356 356
 FT TURN 357 357
 FT STRAND 365 365
 FT TURN 370 370
 FT TURN 371 371
 FT STRAND 372 372
 FT TURN 373 373
 FT TURN 378 378
 FT TURN 381 381
 FT TURN 382 382
 FT TURN 387 387
 FT TURN 397 397
 FT TURN 400 400
 FT HELIX 403 403
 FT HELIX 412 412
 FT HELIX 419 419
 FT TURN 423 423
 FT TURN 424 424
 FT TURN 426 426
 FT HELIX 435 435
 FT TURN 447 447
 FT TURN 447 447
 FT TURN 447 447
 FT TURN 457 457
 FT TURN 459 459
 FT TURN 460 460
 FT STRAND 463 463
 FT TURN 470 470
 FT TURN 474 474
 FT TURN 476 476
 FT STRAND 481 481
 FT TURN 482 482
 FT TURN 485 485
 FT HELIX 486 486
 FT TURN 490 490
 FT TURN 491 491
 FT TURN 495 495
 FT TURN 497 497
 FT HELIX 510 510
 FT TURN 513 513
 FT TURN 514 514


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Query Match      25.8%; Score 49.5; DB 1; Length 847;
Best Local Similarity 33.3%; Pred. No. 36;
Matches 11; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 4 FWGDTLNCWM-----LSAFSRYARCLAEHGD 29
DB 786 YWGNLLQYIOELKNSAVSLFATAIAVAEGTD 818

RESULT 10
ID APAH_BURMA STANDARD; PRT; 282 AA.
AC Q9AEV8;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)
DE (diadenosine tetraphosphatase) (Ap4A hydrolase) (diadenosine 5',5''-
DE P1,P4-tetraphosphate pyrophosphohydrolase).
GN APAH.
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP SEQUENCE FROM N.A.
RA Burtick M.N., Brett P.J., Woods D.E.;
RT "Physical and molecular characterization of lipopolysaccharide
RT O-antigens from Burkholderia mallei.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Hydrolyzes diadenosine 5',5''-P1,P4-tetraphosphate to
CC yield ADP (By similarity).
CC -1- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
CC H(2)O -> 2 ADP.
CC -1- SIMILARITY: BELONGS TO THE AP4A HYDROLASE FAMILY.
CC
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CC
CC EMBL: AF064070; AAD05453.1; -
CC InterPro: IPR004617; ApAH.
CC InterPro: IPR004843; M-ppetrase.
CC InterPro: IPR004844; S/T-phosphatase.
CC Pfam: PF00149; Metallophos; 1.
CC ProDom: PD000252; S/T-phosphatase; 1.
CC TIGRFAMs: TIGR00668; apah; 1.
CC Hydrolase.
KW
SQ SEQUENCE 282 AA; 30631 MW; 7F83BE3404103374 CRC64;

Query Match      25.5%; Score 49; DB 1; Length 282;
Best Local Similarity 30.2%; Pred. No. 14;
Matches 13; Conservative 2; Mismatches 8; Indels 20; Gaps 2;

QY 5 WGDTL-----NCW-----MLSAFSRYARCLAE 27
DB 151 WRDTRLNNDPNCWSPDLKHADRLRVAFNAFTIRFCTPEG 193

RESULT 11
ID APAH_BURPS STANDARD; PRT; 282 AA.
AC O69115;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)
DE (diadenosine tetraphosphatase) (Ap4A hydrolase) (diadenosine 5',5''-
DE P1,P4-tetraphosphate pyrophosphohydrolase).
GN APAH.
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP SEQUENCE FROM N.A.
RA Burtick M.N., Brett P.J., Woods D.E.;
RT "Physical and molecular characterization of lipopolysaccharide
RT O-antigens from Burkholderia mallei.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Hydrolyzes diadenosine 5',5''-P1,P4-tetraphosphate to
CC yield ADP (By similarity).
CC -1- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
CC H(2)O -> 2 ADP.
CC -1- SIMILARITY: BELONGS TO THE AP4A HYDROLASE FAMILY.
CC
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CC
CC EMBL: AY028370; AAK27390.1; -
CC InterPro: IPR004617; ApAH.
CC InterPro: IPR004843; M-ppetrase.
CC InterPro: IPR004844; S/T-phosphatase.
CC Pfam: PF00149; Metallophos; 1.
CC ProDom: PD000252; S/T-phosphatase; 1.
CC TIGRFAMs: TIGR00668; apah; 1.
CC Hydrolase.
KW
SQ SEQUENCE 282 AA; 30631 MW; 7F83BE3404103374 CRC64;

Query Match      25.5%; Score 49; DB 1; Length 282;
Best Local Similarity 30.2%; Pred. No. 14;
Matches 13; Conservative 2; Mismatches 8; Indels 20; Gaps 2;

QY 5 WGDTL-----NCW-----MLSAFSRYARCLAE 27
DB 151 WRDTRLNNDPNCWSPDLKHADRLRVAFNAFTIRFCTPEG 193

RESULT 11
ID APAH_BURPS STANDARD; PRT; 282 AA.
AC O69115;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)
DE (diadenosine tetraphosphatase) (Ap4A hydrolase) (diadenosine 5',5''-
DE P1,P4-tetraphosphate pyrophosphohydrolase).
GN APAH.
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP SEQUENCE FROM N.A.
RA Burtick M.N., Brett P.J., Woods D.E.;
RT "Physical and molecular characterization of lipopolysaccharide
RT O-antigens from Burkholderia mallei.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Hydrolyzes diadenosine 5',5''-P1,P4-tetraphosphate to
CC yield ADP (By similarity).
CC -1- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
CC H(2)O -> 2 ADP.
CC -1- SIMILARITY: BELONGS TO THE AP4A HYDROLASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF064070; AAD05453.1; -
CC InterPro: IPR004617; ApAH.
CC InterPro: IPR004843; M-ppetrase.
CC InterPro: IPR004844; S/T-phosphatase.
CC Pfam: PF00149; Metallophos; 1.
CC ProDom: PD000252; S/T-phosphatase; 1.
CC TIGRFAMs: TIGR00668; apah; 1.
CC Hydrolase.
KW
SQ SEQUENCE 282 AA; 30609 MW; 5D8BF8335C27F44 CRC64;

Query Match      25.5%; Score 49; DB 1; Length 282;
Best Local Similarity 30.2%; Pred. No. 14;
Matches 13; Conservative 2; Mismatches 8; Indels 20; Gaps 2;

QY 5 WGDTL-----NCW-----MLSAFSRYARCLAE 27
DB 151 WRDTRLNNDPNCWSPDLKHADRLRVAFNAFTIRFCTPEG 193

RESULT 12
ID PEPE_ECOLI STANDARD; PRT; 229 AA.
AC P32666;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidase E (EC 3.4.-.-) (Alpha-aspartyl dipeptidase) (Asp-specific
DE dipeptidase).
GN PEPE OR B4021 OR Z5612 OR ECS4939.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 33334;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=K12 / MG155;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes."
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
```

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GN APAH.
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=28450;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=1026b;
RA DeShazer D., Brett P.J., Woods D.E.;
RT "The type II O-antigen moiety of Burkholderia pseudomallei
RT lipopolysaccharide is required for serum resistance and virulence.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Hydrolyzes diadenosine 5',5''-P1,P4-tetraphosphate to
CC yield ADP (By similarity).
CC -1- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
CC H(2)O -> 2 ADP.
CC -1- SIMILARITY: BELONGS TO THE AP4A HYDROLASE FAMILY.
CC
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CC
CC EMBL: AF064070; AAD05453.1; -
CC InterPro: IPR004617; ApAH.
CC InterPro: IPR004843; M-ppetrase.
CC InterPro: IPR004844; S/T-phosphatase.
CC Pfam: PF00149; Metallophos; 1.
CC ProDom: PD000252; S/T-phosphatase; 1.
CC TIGRFAMs: TIGR00668; apah; 1.
CC Hydrolase.
KW
SQ SEQUENCE 282 AA; 30609 MW; 5D8BF8335C27F44 CRC64;

Query Match      25.5%; Score 49; DB 1; Length 282;
Best Local Similarity 30.2%; Pred. No. 14;
Matches 13; Conservative 2; Mismatches 8; Indels 20; Gaps 2;

QY 5 WGDTL-----NCW-----MLSAFSRYARCLAE 27
DB 151 WRDTRLNNDPNCWSPDLKHADRLRVAFNAFTIRFCTPEG 193

RESULT 12
ID PEPE_ECOLI STANDARD; PRT; 229 AA.
AC P32666;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidase E (EC 3.4.-.-) (Alpha-aspartyl dipeptidase) (Asp-specific
DE dipeptidase).
GN PEPE OR B4021 OR Z5612 OR ECS4939.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 33334;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=K12 / MG155;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes."
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
```

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RMD 0509952;
RX MEDLINE-21156231; PubMed-11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.,
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
CC -I- FUNCTION: Hydrolyzes dipeptides containing N-terminal aspartate
residues. May play a role in allowing the cell to use peptide
aspartate to spare carbon otherwise required for the synthesis of
the aspartate family of amino acids.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S51.
CC -----
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CC -----
DR EMBL: U00006; AAC43115.1; -
DR EMBL: AE000475; AAC76991.1; -
DR EMBL: AE005634; AG59213.1; -
DR EMBL: AP002567; BAB38362.1; -
DR HSP: P36936; IFYE.
DR MEROPS: S51.001; -
DR EcoGene: EG11920; pepE.
DR InterPro: IPR005320; Peptidase_S51.
DR Pfam: PF03575; Peptidase_S51; 1.
KW Hydrolyase; Serine protease; Dipeptidase; Complete proteome.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 135 135 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 157 157 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 229 AA; 24570 MW; 53D4D8395DFC63FD CRC64;
Query Match 25.0%; Score 48; DB 1; Length 229;
Best Local Similarity 37.0%; Pred. No. 16;
Matches 10; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 7 DTLCNWLNSAFSRYARCLAEHGDPQTQ 33
Db 145 DALNLPPLQINPHTNALPEGHGKETR 171
RESULT 13
HEAD_BPGAL STANDARD; PRT; 472 AA.
AC Q9FZW7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Major head protein.
GN 8.
OS Bacteriophage GA-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
OX NCBI_TaxID=12345;
RN [1]
RP SEQUENCE FROM N.A.
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RA Meijer W.J.J., Horcajadas J.A., Salas M.;
RT "The phi29 family of phages";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: X96987; CAC21529.1; -
SQ SEQUENCE 472 AA; 53022 MW; 3104821153B1C4C2 CRC64;
Query Match 25.0%; Score 48; DB 1; Length 472;
Best Local Similarity 33.3%; Pred. No. 32;
Matches 8; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 2 GTFGDTLCNWLNSAFSRYARCLAE 25
Db 318 GWYNYLHWQVLSSTREANAVA 341
RESULT 14
AGRI_RAT STANDARD; PRT; 1959 AA.
AC P25304; Q63034;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agrin precursor.
GN AGRN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-1779 AND 1799-1959 FROM N.A.
RC TISSUE-Embryonic spinal cord;
RX MEDLINE-91222570; PubMed-1851019;
RA Rupp F., Payan D.G., Magill-Solc C., Cowan D.M., Scheller R.H.;
RT "Structure and expression of a rat agrin";
RL Neuron 6:811-823(1991).
RN [2]
RP SEQUENCE OF 1777-1801 FROM N.A.
RX MEDLINE-92407628; PubMed-1326608;
RA Rupp F., Oezcelik T., Linial M., Peterson K., Francke U., Scheller R.;
RT "Structure and chromosomal localization of the mammalian agrin gene";
RL J. Neurosci. 12:3535-3544(1992).
CC -I- FUNCTION: COMPONENT OF THE BASAL LAMINA THAT CAUSES THE
AGGREGATION OF ACETYLCHOLINE RECEPTORS AND ACETYLCHOLINE-ESTERASE
ON THE SURFACE OF MUSCLE FIBERS OF THE NEUROMUSCULAR JUNCTION.
CC -I- SUBUNIT: BINDS TO LAMININ.
CC -I- SUBCELLULAR LOCATION: SYNAPTIC BASAL LAMINA AT THE NEUROMUSCULAR
JUNCTION.
CC -I- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4
AND 5; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR
ACETYLCHOLINE RECEPTOR CLUSTERING ACTIVITY.
CC -I- TISSUE SPECIFICITY: EMBRYONIC NERVOUS SYSTEM AND MUSCLE.
CC -I- DEVELOPMENTAL STAGE: MORE ABUNDANT EARLY IN DEVELOPMENT.
CC -I- PTM: CONTAINS HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-
LINKED OLIGOSACCHARIDES (BY SIMILARITY).
CC -I- SIMILARITY: CONTAINS 9 KAZAL-LIKE DOMAINS.
CC -I- SIMILARITY: CONTAINS 2 LAMININ EGF-LIKE DOMAINS.
CC -I- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -I- SIMILARITY: CONTAINS 1 SEA DOMAIN.
CC -I- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
CC -I- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-18 OR MET-24 IS THE
INITIATOR.
CC -----
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OM protein - protein search, using sw model

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(without alignments)
79.311 Million cell updates/sec

Title: US-09-989-481-4
Perfect score: 192
Sequence: 1 LGTFWGTLCNWMLSAFSRYARCLAEHGDPQ 33
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	30.7	910	2 T38539	probable Importin
2	56.5	29.4	223	2 D70760	hypothetical prote
3	55	28.6	694	2 T52574	cyclic nucleotide
4	54	28.1	287	2 T39197	yeast atp12 protei
5	54	28.1	316	2 C87318	hypothetical prote
6	52	27.1	255	2 G87668	conserved hypothet
7	52	27.1	533	2 T01864	hypothetical prote
8	52	27.1	544	2 S41090	triacylglycerol li
9	52	27.1	563	1 ACGUGC	mypl protein - smu
10	51.5	26.8	1150	2 S58775	Ig heavy chain v r
11	51	26.6	90	2 S24248	Ig heavy chain v r
12	51	26.6	101	2 S24257	Ig heavy chain v r
13	51	26.6	105	2 S24249	Ig heavy chain v r
14	51	26.6	109	2 S24254	Ig heavy chain v r
15	51	26.6	109	2 S24253	Ig heavy chain v r
16	51	26.6	110	2 S24250	Ig heavy chain v r
17	51	26.6	113	2 S24247	Ig heavy chain v r
18	51	26.6	373	2 G85355	nodulin-like prote
19	51	26.6	418	2 S11678	cyclin A - African
20	51	26.6	472	2 D75464	probable zinc meta
21	51	26.6	474	2 D91075	6-phospho-beta-glu
22	51	26.6	474	2 C85920	6-phospho-beta-glu
23	51	26.6	474	2 H65051	6-phospho-beta-glu
24	51	26.6	1207	1 EGHU	epidermal growth f
25	50.5	26.3	537	2 T05816	hypothetical prote
26	50	26.0	726	2 T51519	cyclic nucleotide
27	49.5	25.8	355	2 T50479	G protein alpha ch
28	49.5	25.8	408	2 T38386	hypothetical wd-40
29	49	25.5	117	2 T46430	hypothetical prote

30	49	25.5	414	2 H86736	rod-shape determin
31	49	25.5	709	2 D82825	conserved hypothet
32	48.5	25.3	293	2 D95919	hypothetical prote
33	48.5	25.3	506	2 T35261	probable metallope
34	48	25.0	135	2 H71051	hypothetical prote
35	48	25.0	229	2 D65209	peptidase E - Esch
36	48	25.0	229	2 C91246	peptidase E (impor
37	48	25.0	229	2 A86094	peptidase E (impor
38	48	25.0	353	2 AC3320	integral membrane
39	48	25.0	1959	1 AGRT	agrin - rat
40	47.5	24.7	339	2 T05217	protein sam2B - sp
41	47.5	24.7	467	2 G83592	adenosylmethionine
42	47.5	24.7	477	2 T05202	pectinesterase hom
43	47	24.5	102	2 S24260	Ig heavy chain v r
44	47	24.5	115	2 T31781	hypothetical prote
45	47	24.5	241	2 C82852	competence protein

ALIGNMENTS

RESULT 1

T38539

Probable importin beta-2 subunit (transportin) - fission yeast (Schizosaccharomyces p.

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T38539

R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z31748

A:Accession: T38539

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-910 <OLI>

A:Cross-references: EMBL:299165; PIDN:CAB16272.1; GSPDB:GN00066; SPDB:SPAC2F3.06c

A:Experimental source: strain 972h-; cosmid c2F3

C:Genetics:

A:Gene: SPDB:SPAC2F3.06c

A:Map position: 1

A:Introns: 36/3

Query Match 30.7%; Score 59; DB 2; Length 910;
Best Local Similarity 40.9%; Pred. No. 3.7;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 8 TLNCWMLSAFSRYARCLAECHD 29

DB 473 TTTCWTLKRYKWSCLSEED 494

RESULT 2

D70760

hypothetical protein RV2014 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: D70760

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, K.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70760

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-223 <COL>

A:Cross-references: GE:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:el2999

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2014

Query Match 29.4%; Score 56.5; DB 2; Length 223;

[illegible]

Matches 10; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 LGTFWGDTLNCWMLSAFSRYARCLAEHGD 29
|| : : : || : : : || : : : || : : : ||
Db 145 LGQIYKESVNYWMSHRTKLFARHLVGRD 173

RESULT 8

S41090
triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (Geotrichum candidum) (strain ATCC 36614)
A:Species: Geotrichum candidum
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Bartholini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
Eur. J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41090
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02622; NID:g409275; PIDN:AAA03435.1; PID:g409276
A:Experimental source: ATCC 34614
A:Note: Only the translation of the mature protein is shown
C:Genetics:
A:Gene: lipi
C:Function:
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:61-105,276-288/Disulfide bonds: #status predicted
F:217/Active site: Ser #status predicted
F:283,364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 27.1%; Score 52; DB 2; Length 544;
Best Local Similarity 40.0%; Pred. No. 21;
Matches 14; Conservative 1; Mismatches 14; Indels 6; Gaps 1;

QY 1 LGTFWGDTL-----NCWMLSAFSRYARCLAEHGD 29
||||| : : : || : : : || : : : || : : : ||
Db 459 LGTFHGSDDLFOYAGWPWSSSAYRRYFISFANHDD 493

RESULT 9

ACGGUC
triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (Geotrichum candidum)
N:Alternate names: lipase
C:Species: Geotrichum candidum
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Mar-2000
C:Accession: JQ0022
R:Nagao, T.; Shimada, Y.; Sugihara, A.; Tominaga, Y.
J. Biochem. 113, 776-780, 1993
A:Title: Cloning and sequencing of two chromosomal lipase genes from Geotrichum candidum
A:Reference number: PNO492; MUID:93380907; PMID:8370674
A:Accession: PNO492
A:Molecule type: DNA
A:Residues: 1-563 <NAG>
A:Note: The translation of residues 31-350 and the corresponding nucleotide sequence are
R:Shimada, Y.; Sugihara, A.; Tominaga, Y.; Iizumi, T.; Tsunasawa, S.
J. Biochem. 106, 383-388, 1989
A:Title: cDNA molecular cloning of Geotrichum candidum lipase.
A:Reference number: JQ0022; MUID:90110016; PMID:2481674
A:Accession: JQ0022
A:Molecule type: mRNA
A:Residues: 1-563 <SHI>
A:Experimental source: strain ATCC 34614
A:Note: sequences of several small peptides were also determined
C:Comment: The extracellular lipase produced by Geotrichum candidum hydrolyzes all ester
C:Genetics:

A:Gene: lipi
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; pyroglutamic acid
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-563/Product: triacylglycerol lipase #status experimental <MAT>
F:43-560/Domain: cholinesterase homology <CHE>
F:234-238/Region: interfacial lipid recognition (GXSG) motif
F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:80-124,295-307/Disulfide bonds: #status predicted
F:236/Active site: Ser #status predicted
F:302,363/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 27.1%; Score 52; DB 1; Length 563;
Best Local Similarity 40.0%; Pred. No. 22;
Matches 14; Conservative 1; Mismatches 14; Indels 6; Gaps 1;

QY 1 LGTFWGDTL-----NCWMLSAFSRYARCLAEHGD 29
||||| : : : || : : : || : : : || : : : ||
Db 478 LGTFHGSDDLFOYAGWPWSSSAYRRYFISFANHDD 512

RESULT 10

S58775
mypl protein - smut fungus (Ustilago maydis)
C:Species: Ustilago maydis (corn smut)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 21-Jul-2000
C:Accession: S58775
R:Giasson, L.; Kronstad, J.W.
Genetics 141, 491-501, 1995
A:Title: Mutations in the mypl gene of Ustilago maydis attenuate mycelial growth and
A:Reference number: S58775; MUID:96109597; PMID:8647387
A:Accession: S58775
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1150 <GIA>
A:Cross-references: EMBL:L33919; NID:g886415; PIDN:AAC37439.1; PID:g886416
C:Genetics:
A:Gene: mypl

Query Match 26.8%; Score 51.5; DB 2; Length 1150;
Best Local Similarity 39.3%; Pred. No. 53;
Matches 11; Conservative 7; Mismatches 7; Indels 3; Gaps 2;

QY 1 LGTFWGDTLNCWMLSAFSRYARCLAEHGD 28
||||| : : : || : : : || : : : || : : : ||
Db 714 IGTFW-LSRNAWILA--TRGHLLSPGH 738

RESULT 11

S24248
Ig heavy chain V region (VH26) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24248
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B
A:Reference number: S24247
A:Accession: S24248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STE>
A:Cross-references: EMBL:X67069; NID:g38395; PIDN:CAA47454.1; PID:g38396
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.6%; Score 51; DB 2; Length 90;
Best Local Similarity 52.2%; Pred. No. 4.7;
Matches 12; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 LGTFWG--DTLNCWMLSAFSRYA 21
||||| : : : || : : : || : : : || : : : ||
Db 10 LGTAWGVETLCLSLWFTFSYA 32

RESULT 12

S24257
Ig heavy chain V region (VH26-DXP1-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24257
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <STE>
A:Cross-references: EMBL:X67065; PIDN:CAA47450.1; PID:g38388
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-93/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 51; DB 2; Length 101;
Best Local Similarity 52.2%; Pred. No. 5.2;
Matches 12; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 LGTFWG--DTLNCWMLSAFSRYA 21
||||| :||| : ||||
Db 6 LGTAWGVPETLLCSLWFTSSYA 28

RESULT 13

S24249
Ig heavy chain V region (VH26-DN1-DXP1-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C:Accession: S24249
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24249
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <STE>
A:Cross-references: EMBL:X67070
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-92/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 51; DB 2; Length 105;
Best Local Similarity 52.2%; Pred. No. 5.5;
Matches 12; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 LGTFWG--DTLNCWMLSAFSRYA 21
||||| :||| : ||||
Db 5 LGTAWGVPETLLCSLWFTSSYA 27

RESULT 14

S24254
Ig heavy chain V region (VH26-DXP2-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24254
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <STE>
A:Cross-references: EMBL:X67062

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 51; DB 2; Length 109;
Best Local Similarity 52.2%; Pred. No. 5.7;
Matches 12; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 LGTFWG--DTLNCWMLSAFSRYA 21
||||| :||| : ||||
Db 10 LGTAWGVPETLLCSLWFTSSYA 32

RESULT 15

S24253
Ig heavy chain V region (VH26-DLR4-JH6) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24253
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B
A:Reference number: S24247
A:Accession: S24253
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <STE>
A:Cross-references: EMBL:X67061
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-94/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 51; DB 2; Length 109;
Best Local Similarity 52.2%; Pred. No. 5.7;
Matches 12; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 LGTFWG--DTLNCWMLSAFSRYA 21
||||| :||| : ||||
Db 7 LGTAWGVPETLLCSLWFTSSYA 29

Search completed: May 29, 2003, 15:45:53
Job time : 46 secs

; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(328)
; OTHER INFORMATION: Mouse AIPL1 Protein
US-09-765-061B-76

Query Match 27.9%; Score 53.5; DB 9; Length 328;
Best Local Similarity 44.8%; Pred. No. 9.1;
Matches 13; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 4 FWGDTLNCWMLSAFGRYARCLAEHGDGPT 32
|||::: : |||::: |||
Db 87 FWCDDTHGTGVPILSRSLRQMAQKGD-PT 114

SULT 3

US-09-765-061B-74
; Sequence 74, Application US/09765061B
; Publication No. US20030022165A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene 17
; FILE REFERENCE: 96606/16UTL
; CURRENT APPLICATION NUMBER: US/09/765,061B
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Papio anubis
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(372)
; OTHER INFORMATION: Baboon AIPL1 Protein
US-09-765-061B-74

Query Match 27.9%; Score 53.5; DB 9; Length 372;
Best Local Similarity 40.0%; Pred. No. 10;
Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 4 FWGDTLNCWMLSAFGRYARCLAEHGDGPT 33
|||::: : |||::: |||
Db 87 FWCDDTHGTGVPILSRSLRQMAQKGD-PT 115

RESULT 4

US-09-765-061B-78
; Sequence 78, Application US/09765061B
; Publication No. US20030022165A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene 17
; FILE REFERENCE: 96606/16UTL
; CURRENT APPLICATION NUMBER: US/09/765,061B
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Saimiri sciureus
; FEATURE:
; NAME/KEY: PEPTIDE

; LOCATION: (1)..(372)
; OTHER INFORMATION: Squirrel Monkey AIPL1 Protein
US-09-765-061B-78

Query Match 27.9%; Score 53.5; DB 9; Length 372;
Best Local Similarity 40.0%; Pred. No. 10;
Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 4 FWGDTLNCWMLSAFGRYARCLAEHGDGPT 33
|||::: : |||::: |||
Db 87 FWCDDTHGTGVPILSRSLRQMAQKGD-PT 115

RESULT 5

US-09-765-061B-72
; Sequence 72, Application US/09765061B
; Publication No. US20030022165A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene
; FILE REFERENCE: 96606/16UTL
; CURRENT APPLICATION NUMBER: US/09/765,061B
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(384)
; OTHER INFORMATION: Human AIPL1 Protein
; NAME/KEY: misc_feature
; LOCATION: (322)..(322)
; OTHER INFORMATION: Xaa represents any of the twenty amino acids
US-09-765-061B-72

Query Match 27.9%; Score 53.5; DB 9; Length 384;
Best Local Similarity 40.0%; Pred. No. 11;
Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 4 FWGDTLNCWMLSAFGRYARCLAEHGDGPT 33
|||::: : |||::: |||
Db 87 FWCDDTHGTGVPILSRSLRQMAQKGD-PT 115

RESULT 6

US-09-765-061B-73
; Sequence 73, Application US/09765061B
; Publication No. US20030022165A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene
; FILE REFERENCE: 96606/16UTL
; CURRENT APPLICATION NUMBER: US/09/765,061B
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(384)
; OTHER INFORMATION: Chimpanzee AIPL1 Protein
US-09-765-061B-73

Query Match 27.9%; Score 53.5; DB 9; Length 384;
Best Local Similarity 40.0%; Pred. No. 11;

Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;
 QY 4 FWGDTLNCWMLSAFSRYARCLAEHGDGPTQ 33
 || ||:: || |::| ||:
 Db 87 FWCDTHTGVPILSRSLRMAQGRD-PTE 115

RESULT 7
 US-09-765-061B-77
 ; Sequence 77, Application US/09765061B
 ; Publication No. US20030022165A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene 17
 ; FILE OF INVENTION: leber congenital amaurosis (LCA4)
 ; FILE REFERENCE: 96606/16UTL
 ; CURRENT APPLICATION NUMBER: US/09/765, 061B
 ; CURRENT FILING DATE: 2001-01-17
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 77
 ; LENGTH: 392
 ; TYPE: PRT
 ; ORGANISM: Macaca mulatta
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(392)
 ; OTHER INFORMATION: Rhesus Monkey AIPL1 Protein
 US-09-765-061B-77

Query Match 27.9%; Score 53.5; DB 9; Length 392;
 Best Local Similarity 40.0%; Pred. No. 11;
 Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 4 FWGDTLNCWMLSAFSRYARCLAEHGDGPTQ 33
 || ||:: || |::| ||:
 Db 87 FWCDTHTGVPILSRSLRMAQGRD-PTE 115

RESULT 8
 US-09-764-891-3081
 ; Sequence 3081, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3081
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (12)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-764-891-3081

Query Match 26.6%; Score 51; DB 9; Length 56;
 Best Local Similarity 57.9%; Pred. No. 3;
 Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 9 LNCWMLSAFSRYAR--CLA 25
 |||| || | | ||
 Db 25 LNCWHLSCFNHALRLSCLA 43

RESULT 9
 US-09-908-711-83

; Sequence 83, Application US/09908711
 ; Patent No. US20020045230A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA128
 ; CURRENT APPLICATION NUMBER: US/09/908,711
 ; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: US01/01360
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,867
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01344
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,892
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01345
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,888
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01329
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,905
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01354
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,891
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01339
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,869
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01340
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,898
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01320
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,853
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01349
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,902
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01239
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,870
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01348
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,882
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01347
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,896
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01307
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,864
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01341
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,856
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01336
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/764,868
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US01/01312

;; PRIOR FILING DATE: 2001-01-17
;; PRIOR APPLICATION NUMBER: 60/179,065
;; PRIOR FILING DATE: 2000-01-31
;; PRIOR APPLICATION NUMBER: 60/180,628
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: 60/209,467
;; PRIOR FILING DATE: 2000-06-07
;; NUMBER OF SEQ ID NOS: 167
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 83
;; LENGTH: 56
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (12)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-908-711-83

Query Match 26.6%; Score 51; DB 10; Length 56;
Best Local Similarity 57.9%; Pred. No. 3;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

9 LNCWMLSAFSRYAR--CLA 25
||||| | | | |
25 LNCWHLSCFNHALRLSCLA 43

RESULT 10
US-09-815-242-10270
; Sequence 10270, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard

;; TITLE OF INVENTION: Identification of Essential Genes in
;; TITLE OF INVENTION: Prokaryotes

;; FILE REFERENCE: ELITRA.011a
;; CURRENT APPLICATION NUMBER: US/09/815,242

;; CURRENT FILING DATE: 2001-03-21

;; PRIOR APPLICATION NUMBER: 60/191,078

;; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: 60/206,848

;; PRIOR FILING DATE: 2000-03-23

;; PRIOR APPLICATION NUMBER: 60/207,727

;; PRIOR FILING DATE: 2000-05-26

;; PRIOR APPLICATION NUMBER: 60/242,578

;; PRIOR FILING DATE: 2000-10-23

;; PRIOR APPLICATION NUMBER: 60/253,625

;; PRIOR FILING DATE: 2000-11-27

;; PRIOR APPLICATION NUMBER: 60/257,931

;; PRIOR FILING DATE: 2000-12-22

;; PRIOR APPLICATION NUMBER: 60/269,308

;; PRIOR FILING DATE: 2001-02-16

;; NUMBER OF SEQ ID NOS: 14110

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 10270

;; LENGTH: 474

;; TYPE: PRT

;; ORGANISM: Escherichia coli

US-09-815-242-10270

Query Match 26.6%; Score 51; DB 10; Length 474;
Best Local Similarity 43.3%; Pred. No. 31;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

1 LGTFWGDTLNCWMLSAFSRYARCLAEHG 30

Db 141 LVTEYGSWRNRKLVVEFFSRYARTCFEAFDG 170
| | : | | : | | | | | | | | | |

RESULT 11

US-09-476-242-2

; Sequence 2, Application US/09476242

; Patent No. US2002014683A1

; GENERAL INFORMATION:

;; APPLICANT: BARNETT, Susan

;; APPLICANT: HARTOG, Karin

;; APPLICANT: MARTIN, Eric

;; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES

;; FILE REFERENCE: 1605.002

;; CURRENT APPLICATION NUMBER: US/09/476,242

;; CURRENT FILING DATE: 1999-12-30

;; NUMBER OF SEQ ID NOS: 26

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 2

;; LENGTH: 847

;; TYPE: PRT

;; ORGANISM: Human immunodeficiency virus

US-09-476-242-2

Query Match 25.8%; Score 49.5; DB 10; Length 847;

Best Local Similarity 33.3%; Pred. No. 96;

Matches 11; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 4 FWGDTLNCWM-----LSAFSRYARCLAEHGD 29
: | | : | | : | | | | | | | |

Db 786 YGNNLQYWIQELKNSAVSLFDAIAVAEGTD 818
: | | : | | : | | | | | | | |

RESULT 12

US-09-851-138-80

; Sequence 80, Application US/09851138

; Publication No. US20020183508A1

; GENERAL INFORMATION:

;; APPLICANT: MAERTENS, GEERT

;; STUYVER, LIEVEN

;; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC AGENTS

;; NUMBER OF SEQUENCES: 207

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: ARNOLD, WHITE & DURKEE

;; STREET: P. O. BOX 4433

;; CITY: HOUSTON

;; STATE: TEXAS

;; COUNTRY: USA

;; ZIP: 77210-4433

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Microsoft Word 6.0 / ASCII text output

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/851,138

;; FILING DATE: 09-May-2001

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/836,075

;; FILING DATE: <Unknown>

;; APPLICATION NUMBER: EP 94870166.9

;; FILING DATE: 21 Oct 1994

;; APPLICATION NUMBER: EP 95870076.7

;; FILING DATE: 28 Jun 1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: KAMMERER, PATRICIA A.

;; REGISTRATION NUMBER: 29,775

;; REFERENCE/DOCKET NUMBER: INNS:004

;; INFORMATION FOR SEQ ID NO: 80:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 113 amino acids

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-851-138-80

Query Match 25.0%; Score 48; DB 9; Length 113;
Best Local Similarity 36.7%; Pred. No. 17;
Matches 11; Conservative 4; Mismatches 11; Indels 4; Gaps 1;

QY 3 TFWGDTLNCWMLSAFSAFYARCLAECHDGP 32
Db 62 TSMGNTITCYV----KAAACRAAGIDAPT 87

RESULT 13

US-10-210-296-102
; Sequence 102, Application US/10210296
; Publication No. US20030021802A1

GENERAL INFORMATION:

; APPLICANT: Pfizer Products Inc.
; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED
; TITLE OF INVENTION: METHODS
; TITLE OF INVENTION: AND MATERIALS
; FILE REFERENCE: PCI0589A
; CURRENT APPLICATION NUMBER: US/10/210,296
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/689,065
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 102

; LENGTH: 526
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis

US-10-210-296-102

Query Match 25.0%; Score 48; DB 9; Length 526;
Best Local Similarity 40.0%; Pred. No. 93;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 8 TLNCWMLSAFSAFYARCLAECHDGP 32
Db 158 TLNCSTITLLAKSFRSLPEKHGLT 182

RESULT 14

US-10-016-283-34
; Sequence 34, Application US/10016283
; Patent No. US20020164702A1

GENERAL INFORMATION:

; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/016,283
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US/09/077,955A
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US96/20696
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34

; LENGTH: 1940
; TYPE: PRT
; ORGANISM: Rattus. sp.

US-10-016-283-34

Query Match 25.0%; Score 48; DB 9; Length 1940;
Best Local Similarity 39.3%; Pred. No. 3.9e+02;
Matches 11; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 6 GDTLNL--CWMLSAFSAFYARCLAECHDGP 31

Db 328 GHTYNNICWRQQAECROQRAIPPKHGP 355

RESULT 15

US-09-864-761-39145
; Sequence 39145, Application US/09864761
; Patent No. US20020048763A1

GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Asomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39145

; LENGTH: 84

; TYPE: PRT

; ORGANISM: Homo sapiens

FEATURES:

; OTHER INFORMATION: MAP TO AC004691.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EST_HUMAN HIT: AW470102.1, EVALUATE 4.30e-01
; OTHER INFORMATION: SWISSPROT HIT: P01842, EVALUATE 1.90e+00

US-09-864-761-39145

Query Match 24.7%; Score 47.5; DB 10; Length 84;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 6; Indels 11; Gaps 2;

Qy 1 LGTFWGDTLNCWMLSAFSRYARCLAEHGDG 30
| | | | | : | | | |
Db 50 LDPFW-AISCW-----KCHVEPHDG 68

Search completed: May 29, 2003, 15:54:15
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:42:00 ; Search time 27 Seconds
(without alignments)
35.961 Million cell updates/sec

Title: US-09-989-481-4

-Perfect score: 192

Sequence: 1 LGTFWGTLCNCWMLSAFSRYARCLAEHGDGPTQ 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	100.0	33	4	US-08-928-862-4
2	51	26.6	465	4	US-08-914-375C-60
3	48	25.0	113	4	US-08-836-075A-80
4	48	25.0	1940	2	US-08-644-271-30
5	48	25.0	1940	4	US-09-077-955-34
6	47.5	24.7	865	4	US-09-612-204B-24
7	46.5	24.2	243	3	US-09-191-647-14
8	46.5	24.2	243	4	US-09-540-245A-14
9	46.5	24.2	243	4	US-09-540-153-14
10	46.5	24.2	771	4	US-09-188-930-183
11	46.5	24.2	1525	3	US-09-191-647-2
12	46.5	24.2	1525	4	US-09-540-245A-2
13	46.5	24.2	1525	4	US-09-540-153-2
14	45.5	23.7	196	4	US-09-129-030-28
15	45	23.4	2860	4	US-08-826-267-2
16	44.5	23.2	270	4	US-09-399-913-59
17	44.5	23.2	401	1	US-08-368-803-7
18	44.5	23.2	422	2	US-08-663-566A-5
19	44.5	23.2	422	2	US-08-023-610-5
20	44.5	23.2	422	2	US-08-288-065A-5
21	44.5	23.2	422	2	US-08-362-240A-5
22	44.5	23.2	422	4	US-08-804-372A-3
23	44.5	23.2	422	5	PCT-US95-10245-5
24	44	22.9	113	4	US-08-836-075A-78
25	44	22.9	222	6	5223425-6
26	44	22.9	228	4	US-08-944-483-44
27	44	22.9	238	6	5223425-5

28	44	22.9	250	6	5223425-4	Patent No. 5223425
29	44	22.9	253	6	5223425-8	Patent No. 5223425
30	44	22.9	425	1	US-08-190-802A-48	Sequence 48, Appl
31	44	22.9	425	4	US-08-477-346-48	Sequence 48, Appl
32	44	22.9	425	4	US-08-473-089-48	Sequence 48, Appl
33	44	22.9	425	4	US-08-487-072A-48	Sequence 107, App
34	43.5	22.7	178	3	US-08-906-769-107	Sequence 107, App
35	43.5	22.7	178	3	US-08-906-616-107	Sequence 107, App
36	43.5	22.7	178	4	US-08-817-795-107	Sequence 107, App
37	43.5	22.7	178	4	US-08-639-075A-107	Sequence 107, App
38	43.5	22.7	178	4	US-09-012-431-107	Sequence 107, App
39	43.5	22.7	178	4	US-09-012-692-107	Sequence 107, App
40	43.5	22.7	178	4	US-08-906-613-107	Sequence 107, App
41	43.5	22.7	178	5	PCT-US95-14442A-107	Sequence 107, App
42	43.5	22.7	225	4	US-09-004-731-13	Sequence 13, Appl
43	43.5	22.7	225	4	US-08-749-699-13	Sequence 13, Appl
44	43.5	22.7	225	4	US-09-004-729-13	Sequence 13, Appl
45	43.5	22.7	228	4	US-09-004-731-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-928-862-4

; Sequence 4, Application US/08928862

; Patent No. 6309877

; GENERAL INFORMATION:

; APPLICANT: Chau, Raymond M. W.

; TITLE OF INVENTION: Isolation and Use of Motoneuronotrophic Factors

; FILE REFERENCE: 12592-2

; CURRENT APPLICATION NUMBER: US/08/928.862

; CURRENT FILING DATE: 1997-09-12

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 33

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-928-862-4

Query Match 100.0%; Score 192; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 2e-20;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LGTFWGTLCNCWMLSAFSRYARCLAEHGDGPTQ 33

Db 1 LGTFWGTLCNCWMLSAFSRYARCLAEHGDGPTQ 33

RESULT 2

US-08-914-375C-60

; Sequence 60, Application US/08914375C

; Patent No. 6377893

; GENERAL INFORMATION:

; APPLICANT: Steven A. Benner

; FILE REFERENCE: Applications of Protein Structure Predictions

; NUMBER OF SEQUENCES: 74

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Steven A. Benner

; STREET: 1501 NW 68th Terrace

; CITY: Gainesville

; STATE: FL

; COUNTRY: United States

; ZIP: 32605-4147

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: MacIntosh 7.0

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/914.375C

; FILING DATE: 19-Aug-1997

; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 243
; TYPE: PRT
; ORGANISM: mouse
US-09-540-153-14

Query Match 24.2%; Score 46.5; DB 4; Length 243;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 11 CWMLSAFSRYARCLAEHGDG 30
| :||| :||| |
Db 99 CLPINFASYCKCL-EGHGG 117

RESULT 10-
US-09-188-930-183
; Sequence 183, Application US/09188930A
; Patent No. 6150502

GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011C1
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 183
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (717)...(717)
US-09-188-930-183

Query Match 24.2%; Score 46.5; DB 4; Length 771;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 11 CWMLSAFSRYARCLAEHGDG 30
| :||| :||| |
Db 628 CLPINFASYCKCL-EGHGG 646

RESULT 11
US-09-191-647-2
; Sequence 2, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

; LENGTH: 1525
; TYPE: PRT
; ORGANISM: human
US-09-191-647-2

Query Match 24.2%; Score 46.5; DB 3; Length 1525;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 11 CWMLSAFSRYARCLAEHGDG 30
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Db 1381 CLPINFASYCKCL-EGHGG 1399

RESULT 12
US-09-540-245A-2
; Sequence 2, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: human
US-09-540-245A-2

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Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 11 CWMLSAFSRYARCLAEHGDG 30
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Db 1381 CLPINFASYCKCL-EGHGG 1399

RESULT 13
US-09-540-153-2
; Sequence 2, Application US/09540153
; Patent No. 6270995
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,153
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/191,647
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
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; TYPE: PRT
; ORGANISM: human
US-09-540-153-2

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Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 11 CWMLSAFSRYARCLAEHGDG 30
Db 1381 CLPINFASYSCKRL-EGHGG 1399

RESULT 14

US-09-129-030-28
; Sequence 28, Application US/09129030A
; Patent No. 6242221
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
; TITLE OF INVENTION: GENOMIC PPO CLONES
; FILE REFERENCE: 57072-PCT-US
; CURRENT APPLICATION NUMBER: US/09/129,030A
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: AU PN7856
; EARLIER FILING DATE: 1996-02-05
; EARLIER APPLICATION NUMBER: AU P02361
; EARLIER FILING DATE: 1996-09-16
; EARLIER APPLICATION NUMBER: PCT/AU97/00041
; EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: APPLE
US-09-129-030-28

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; Sequence 2, Application US/08826267
; Patent No. 5994070
; GENERAL INFORMATION:
; APPLICANT: Streuli, Michel
; TITLE OF INVENTION: No. 5994070e1 TRIO Molecules and Uses Related Thereto
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,267
; FILING DATE: 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,214
; FILING DATE: 27 MARCH (1996)
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-010

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2860 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-826-267-2

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Search completed: May 29, 2003, 15:46:26
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:33:30 ; Search time 69 Seconds
(without alignments)
63.729 Million cell updates/sec

Title: US-09-989-481-4

Perfect score: 192

Sequence: 1 LGTFWDTLNCWLSAFSRVACRLAEGHDGPTQ 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	192	100.0	33	AAW59046	Human MNTF1-F6 pro
2	56.5	29.4	584	AAW90949	Comamonas testoste
3	55.5	28.9	227	AAU19525	Human diagnostic a
4	55	28.6	694	AAW93813	Herbicidally activ
5	53.5	27.9	326	AAW23939	Hepatitis B virus
6	53.5	27.9	384	AAW94802	Human protein sequ
7	53	27.6	794	AAW25667	Novel human diagno
8	52	27.1	563	AAW10330	Gene product with
9	51	26.6	56	ABG60253	Human ovarian anti
10	51	26.6	56	AAW94423	Human reproductive

11	51	26.6	56	23	ABG61724	Novel ovarian rela
12	51	26.6	466	23	AAE23630	Escherichia coli 6
13	51	26.6	474	22	AAU34677	E. coli cellular p
14	51	26.6	1207	22	AAW78524	Human protein SEQ
15	51	26.6	1207	22	AAW84604	Amino acid sequenc
16	51	26.6	1222	22	ABW11946	Human precursor pr
17	51	26.6	1222	22	AAW79508	Human protein SEQ
18	51	26.6	1225	22	ABG24444	Novel human diagno
19	51	26.6	1258	22	ABG24819	Novel human diagno
20	50	26.0	726	22	ABG68590	ATCNGC2/DND1 prote
21	50	26.0	726	23	ABW93489	Herbicidally activ
22	50	26.0	844	22	ABW61902	Drosophila melanog
23	49.5	25.8	842	23	ABW60211	HIV Env isolate SF
24	49.5	25.8	847	21	AAW97073	Variant HIV-1 SF16
25	49.5	25.8	1054	22	ABW60410	Drosophila melanog
26	49	25.5	414	23	ABW54212	Lactococcus lactis
27	49	25.5	665	19	AAW54425	Human PS12 protei
28	49	25.5	665	21	AAW08415	Protein encoded by
29	48.5	25.3	150	22	AAU87494	Novel central nerv
30	48	25.0	94	22	ABG19025	Novel human diagno
31	48	25.0	113	17	AAW96565	Hepatitis C virus
32	48	25.0	116	22	ABG30144	Novel human diagno
33	48	25.0	526	22	AAW78608	Lawsonia intracell
34	48	25.0	731	22	ABG30155	Novel human diagno
35	48	25.0	743	23	ABW92349	Herbicidally activ
36	48	25.0	839	23	AAE23384	Human intracellular
37	47.5	24.7	84	22	ABW38826	Peptide #6332 enco
38	47.5	24.7	84	22	ABW23847	Protein #5846 enco
39	47.5	24.7	84	22	AAW59470	Human brain expres
40	47.5	24.7	84	22	AAW72034	Human bone marrow
41	47.5	24.7	84	22	AAW19413	Peptide #5847 enco
42	47.5	24.7	84	22	AAW32300	Peptide #6337 enco
43	47.5	24.7	84	23	ABG41849	Human peptide enco
44	47.5	24.7	273	23	ABW91902	Herbicidally activ
45	47.5	24.7	433	21	AAW50117	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAW59046
ID AAW59046 standard; Protein; 33 AA.

XX AC AAW59046;

XX DT 11-AUG-1998 (first entry)

XX DE Human MNTF1-F6 protein fragment.

XX KW Motoneuronotrophic factor; MNTF-1; MNTF1-F6; human; axon regeneration;
KW motoneuron; diagnose; treatment; disease; wound healing; scar tissue;
KW keloid.

XX OS Homo sapiens.

XX PN WO9813492-A2.

XX PD 02-APR-1998.

XX PF 22-SEP-1997; 97WO-US17142.

XX PR 12-SEP-1997; 97US-0928862.

XX PR 27-SEP-1996; 96US-0026792.

XX PR 15-NOV-1996; 96US-0751225.

XX PA (KMBI-) KM BIOTECH INC.

XX PI Chau RMW;

XX WPI; 1998-230705/20.

XX DR N-PSDB; AAW1174E.

XX XX

PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 06-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465570/50.

N-PSDB; AAL00393.

Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition -

Claim 11; SEQ ID NO 3081; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.

Sequence 56 AA;

Query Match 26.6%; Score 51; DB 22; Length 56;

Best Local Similarity 57.9%; Pred. No. 15;

Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Oy 9 LNCWMLSAFSRYAR-CLA 25

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25 LNCWHLSCFNHALRLSCLA 43

RESULT 11

ABG61724

ID ABG61724 standard; Protein: 56 AA.

XX AC ABG61724;

DT 26-AUG-2002 (first entry)

DE Novel ovarian related polypeptide #15.

XX Ovarian related polypeptide; neoplastic disorder; tumour; ovarian cancer;
 KW hyperproliferative disorder; adult acute lymphocytic leukaemia;
 KW breast cancer; reproductive system disorder; tuberculosis; arthritis;
 KW immune system disorder; Chediak-Higashi's syndrome; neonatal neutropenia;
 KW autoimmune disorder; Hashimoto's thyroiditis; inflammatory disorder;
 KW septic shock; multiple sclerosis; central nervous system disorder;
 KW neurological disorder; allergy; Parkinson's disease; Alzheimer's disease;
 KW cardiovascular disorder; atherosclerosis; blood related disorder;
 KW respiratory disorder; urinary system disorder; musculoskeletal disorder;
 KW osteoporosis; wound healing; endocrine disorder; infectious disease;
 KW gastrointestinal disorder; transplantation; food additive; preservative.

OS Homo sapiens.

XX US2002045230-A1.

FN

XX 18-APR-2002.
 PD 20-JUL-2001; 2001US-0908711.
 XX 31-JAN-2000; 2000US-179065P.
 PR 04-FEB-2000; 2000US-180628P.
 PR 24-FEB-2000; 2000US-184664P.
 PR 02-MAR-2000; 2000US-186350P.
 PR 16-MAR-2000; 2000US-189874P.
 PR 17-MAR-2000; 2000US-190076P.
 PR 18-APR-2000; 2000US-198123P.
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 PR 07-JUN-2000; 2000US-209467P.
 PR 28-JUN-2000; 2000US-214886P.
 PR 30-JUN-2000; 2000US-215135P.
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PR 11-DEC-2000; 2000US-254057P.
PR 05-JAN-2001; 2001US-259678P.
PR 17-JAN-2001; 2001US-0764853.
PR 17-JAN-2001; 2001US-0764856.
PR 17-JAN-2001; 2001US-0764864.
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PR 17-JAN-2001; 2001US-0764882.
PR 17-JAN-2001; 2001US-0764888.
PR 17-JAN-2001; 2001US-0764891.
PR 17-JAN-2001; 2001US-0764892.
PR 17-JAN-2001; 2001US-0764896.
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PR 17-JAN-2001; 2001US-0764905.
PR 17-JAN-2001; 2001WO-US01239.
PR 17-JAN-2001; 2001WO-US01307.
PR 17-JAN-2001; 2001WO-US01312.
PR 17-JAN-2001; 2001WO-US01320.
PR 17-JAN-2001; 2001WO-US01329.
PR 17-JAN-2001; 2001WO-US01334.
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PR 17-JAN-2001; 2001WO-US01339.
PR 17-JAN-2001; 2001WO-US01340.
PR 17-JAN-2001; 2001WO-US01341.
PR 17-JAN-2001; 2001WO-US01344.
PR 17-JAN-2001; 2001WO-US01345.
PR 17-JAN-2001; 2001WO-US01347.
PR 17-JAN-2001; 2001WO-US01348.
PR 17-JAN-2001; 2001WO-US01360.
XX
PA. (ROSE/) ROSEN C A.
PA. (RUBI/) RUBIN S M.
PA. (BARA/) BARASH S C.
XX

Query Match 26.6%; Score 51; DB 23; Length 56;
Best Local Similarity 57.9%; Pred. No. 15;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 9 LNCWMLSAFSRYAR--CLA 25
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Db 25 LNCWHLSCFNHALRLSCLA 43

RESULT 12

AAE23630
ID AAE23630 standard; Protein; 466 AA.

XX AC AAE23630;

XX DT 27-AUG-2002 (first entry)

XX DE Escherichia coli 6-phospho-strand-glucosidase #1.

XX KW Secondary structural element; genome-sized database; EC 3.2.1.86;

XX OS Escherichia coli.

XX FT Key Location/Qualifiers
FT Region 9..11
FT /note= "Strand A"
FT Region 12..103
FT /note= "GG dipeptide parse"
FT Region 14..20
FT /note= "Strand B"
FT Region 48..59
FT /note= "Parse region"
FT Region 49..51
FT /note= "Strand A"
FT Region 50..54
FT /note= "Parsing string (PGDSC)"
FT Region 53..60
FT /note= "Strand B"
FT Region 62..63
FT /note= "GG dipeptide parse"

CC invention.
XX
SQ Sequence 466 AA;
Query Match 26.6%; Score 51; DB 23; Length 466;
Best Local Similarity 43.3%; Pred. No. 1.5e+02;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 1 LGTFWGDYLNWMLSAFSAFYARCLAEHGDG 30
DB 138 LVTEYGSWRNRLKLVFFSRYARTCFEAFDG 167

RESULT 13
AAU34677
ID AAU34677 standard; Protein; 474 AA.
XX
AC AAU34677;
XX
DT 14-FEB-2002 (first entry)
XX
DE E. coli cellular proliferation protein #258.
XX
KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
OS Escherichia coli.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Travick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI: 2001-611495/70.
DR N-PSDB; AAS52536.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 10270; 511pp; English.

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 474 AA;
Query Match 26.6%; Score 51; DB 22; Length 474;
Best Local Similarity 43.3%; Pred. No. 1.5e+02;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 1 LGTFWGDYLNWMLSAFSAFYARCLAEHGDG 30
DB 141 LVTEYGSWRNRLKLVFFSRYARTCFEAFDG 170

RESULT 14
AAU78524
ID AAU78524 standard; Protein; 1207 AA.
XX
AC AAU78524;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1186.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PSDB; AAK51657.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 3434-3436; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAU78323-AAU80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAU80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.

XX SQ Sequence 1207 AA;

Query Match 26.6%; Score 51; DB 22; Length 1207;
Best Local Similarity 56.2%; Pred. No. 4.1e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 18 SRVARCIAEGHGDGPTQ 33
| | | | | : | | | | |
Db 841 SMYARCISEGEDATCQ 856

RESULT 15
AAB84604
ID AAB84604 standard; Protein; 1207 AA.

XX AC AAB84604;

XX 05-SEP-2001 (first entry)

XX Amino acid sequence of endothelial growth factor.

XX Growth factor; protein inhibitor; protease; damaged tissue;
XX platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
XX connective tissue derived growth factor; CTGF; chrysalin; VEGF;
XX keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
XX transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
XX granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
XX vascular endothelial growth factor; urokinase plasminogen activator;
XX dermal ulcer; wound.

XX Homo sapiens.

XX WO200149309-A2.

XX 12-JUL-2001.

XX 21-DEC-2000; 2000WO-IB01935.

XX 29-DEC-1999; 99GB-0030768.

XX (PFI2) PFIZER LTD.
XX (PFI2) PFIZER INC.

XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;

XX WPI; 2001-418351/44.
XX N-PSDB; AAH28219.

XX Composition for the treatment of damaged tissue i.e. chronic wounds and
XX dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
XX factor .

XX Disclosure; Page 549; 572pp; English.

XX The specification describes a pharmaceutical composition, comprising
XX a growth factor, an inhibitor agent, i.e. a protease. The inhibitor
XX agent inhibits the action of at least one specific adverse protein,
XX i.e. a protease, that is upregulated in a damaged tissue such as a
XX wound environment. Growth factors which are included in the composition
XX of the invention are platelet-derived growth factor (PDGF), fibroblast
XX growth factor (FGF), connective tissue derived growth factor (CTGF),
XX keratinocyte-derived growth factor (KGF), transforming growth
XX factor-beta (TGF-beta), granulocyte macrophage colony stimulating factor
XX (GM-CSF), epidermal growth factor (EGF), vascular endothelial growth
XX factor (VEGF), and chrysalin. Inhibitors which are included in the
XX composition of the invention include inhibitors of urokinase-type
XX plasminogen activator (uPA) and matrix metalloproteinase (MMP). The
XX composition is useful for the treatment of chronic damaged tissue, i.e.
XX wounds and dermal ulcers. The present sequence represents a human EGF,
XX and is used to produce the composition of the invention.

XX Sequence 1207 AA;

Query Match 26.6%; Score 51; DB 22; Length 1207;
Best Local Similarity 56.2%; Pred. No. 4.1e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY 18 SRVARCIAEGHGDGPTQ 33
| | | | | : | | | | |
Db 841 SMYARCISEGEDATCQ 856

Search completed: May 29, 2003, 15:43:06
Job time : 71 secs

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